Figure 1A

```
  1  CCCACGCGTCCGGGGAGCTTGCACTAACATCTACAATGGCTTCTAAAAAGCACAGATGAC   60

 61  CTGCTACACTTCCTGACTTGCTTGCTATTGGTTGGCACTGTTCATAAATATAATTTGCTC  120

121  TTTCACTTTTCTTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA  180

181  GAGGCAGCAGAAGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG  240

241  CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTTGAC  300

301  TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCATTTGAT  360

361  AAGGGAAAACTAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT  420

421  GTGAGCAACGTGGAAGATGGGTGATTTCTGCATTTCCAACTGAGCATGGAGAGAAAAATT  480

481  TATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA  540
  1                                             M   E   P   N   G   T   F   S   N    9

541  TAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTTTTCCCAATTGTATA  600
 10   N   N   S   R   N   C   T   I   E   N   F   K   R   E   F̲   F̲   P̲   I̲   V̲   Y̲   29

601  TCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCCTGCA  660
 30   L̲   I̲   I̲   F̲   F̲   W̲   G̲   V̲   L̲   G̲   N̲   G̲   L̲   S̲   I̲   Y̲   V̲   F̲   L̲   Q   49

661  GCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCT  720
 50   P   Y   K   K   S   T   S   V   N   V̲   F̲   M̲   L̲   N̲   L̲   A̲   I̲   S̲   D̲   L̲   69

721  CCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT  780
 70   L̲   F̲   I̲   S̲   T̲   L̲   P̲   F̲   R̲   A̲   D̲   Y̲   Y̲   L̲   R   G   S   N   W   I   89

781  ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAG  840
 90   F   G   D   L   A   C   R   I   M   S   Y   S   L   Y   V̲   N̲   M̲   Y̲   S̲   S̲  109

841  TATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCG  900
110   I̲   Y̲   F̲   L̲   T̲   V̲   L̲   S̲   V̲   V̲   R̲   F̲   L̲   A̲   M̲   V̲   H   P   F   R  129
```

Figure 1B

```
 901  GCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCT   960
 130    L  L  H  V  T  S  I  R  S  A  W  I  L  C  G  I  I  W  I  L    149

 961  TATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCAC  1020
 150    I  M  A  S  S  I  M  L  L  D  S  G  S  E  Q  N  G  S  V  T   169

1021  ATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGC  1080
 170    S  C  L  E  L  N  L  Y  K  I  A  K  L  Q  T  M  N  Y  I  A   189

1081  CTTGGTGGTGGGCTGCCTGCTGCCATTTTTTCACACTCAGCATCTGTTATCTGCTGATCAT  1140
 190    L  V  V  G  C  L  L  P  F  F  T  L  S  I  C  Y  L  L  I  I   209

1141  TCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGC  1200
 210    R  V  L  L  K  V  E  V  P  E  S  G  L  R  V  S  H  R  K  A   229

1201  ACTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTCCTGCCCTATCACAC  1260
 230    L  T  T  I  I  I  T  L  I  I  F  F  L  C  F  L  P  Y  H  T   249

1261  ACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAA  1320
 250    L  R  T  V  H  L  T  T  W  K  V  G  L  C  K  D  R  L  H  K   269

1321  AGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTA  1380
 270    A  L  V  I  T  L  A  L  A  A  A  N  A  C  F  N  P  L  L  Y   289

1381  TTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCC  1440
 290    Y  F  A  G  E  N  F  K  D  R  L  K  S  A  L  R  K  G  H  P   309

1441  ACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAG  1500
 310    Q  K  A  K  T  K  C  V  F  P  V  S  V  W  L  R  K  E  T  R   329

1501  AGTATAAGGAGCTCTTAGATGAGACCTGTTCTTGTATCCTTGTGTCCATCTTCATTCACT  1560
 330    V  *                                                         331

1561  CATAGTCTCCAAATGACTTTGTATTTACATCACTCCCAACAAATGTTGATTCTTAATATT  1620

1621  TAGTTGACCATTACTTTTGTTAATAAGACCTACTTCAAAAATTTTATTCAGTGTAAAAAA  1680

1681  AAAAAAAAAAAAAAAAAAAAAAAAAAAA  1708
```

Figur 2A

```
              1                                                 50
HGPRBMY11   (1)  -----MSLQPSISVSEMEPNC-----------TFSNNNSRNCTIEN--FK
HGPRBMY11v1 (1)  MERKFMSLQPSISVSEMEPNC-----------TFSNNNSRNCTIEN--FK
P2Y5_CHICK  (1)  ------------------------------MVSSNCSTEDC-FK
P2YR_CHICK  (1)  MTEALISAALNGTQPELLAGC-----------WAAGNATTKCSLTKTGFO
P2YR_MELGA  (1)  MTEALISAALNGTQPELLAGC-----------WAAGNASTKCSLTKTGFO
P2YR_RAT    (1)  MTEVPWSAVPNGTDAAFLAGLGSLWGNSTIASTAAVSSSFRCALIKTGFO
Q9Y271      (1)  ------------------MDETC-----------NLTVSSATCHDTIDDFR
GPRH_HUMAN  (1)  ----------MNGLEVAPPC---------LITNFSLATAEQCGQETPLE

              51                                                100
HGPRBMY11   (22) REFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLE
HGPRBMY11v1 (38) REFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLE
P2Y5_CHICK  (14) YTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTYMLNLAISDLLE
P2YR_CHICK  (40) FYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMLNLALADELY
P2YR_MELGA  (40) FYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMLNLALADELY
P2YR_RAT    (51) FYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMLNLALADELY
Q9Y271      (23) NQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMLNLAVADLLC
GPRH_HUMAN  (31) NMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSC

              101                                               150
HGPRBMY11   (72)  ISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRF
HGPRBMY11v1 (88)  ISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRF
P2Y5_CHICK  (64)  VFTLPFRIYYFVVRN-WPFGDVLCKISVTLFYTNMYGSILFLTCISVDRF
P2YR_CHICK  (90)  VLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRY
P2YR_MELGA  (90)  VLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRY
P2YR_RAT    (101) VLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRY
Q9Y271      (73)  VCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRC
GPRH_HUMAN  (81)  VLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRF

              151                                               200
HGPRBMY11   (122) LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDS---GSEONGSV
HGPRBMY11v1 (138) LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDS---GSEONGSV
P2Y5_CHICK  (113) LAIVHPFRSKTLRTKRNARIVCAWITVLAGSTPASEFQSTNRQNNTEQ
P2YR_CHICK  (140) TGVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTI
P2YR_MELGA  (140) TGVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTI
P2YR_RAT    (151) SGVVYPLKSLGRLKKKNAIYVSVLWLIVVVAISPILFYSGTGIRKNKTV
Q9Y271      (123) IAIVFPVQNINLVTQKKARFVCGIWIFVILTSSPFLMAKPQKDEKNNTK
GPRH_HUMAN  (131) LAIVHPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVV

              201                                               250
HGPRBMY11   (169) ISCLE--LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE
HGPRBMY11v1 (185) ISCLE--LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE
P2Y5_CHICK  (163) RTCFENFPESTWKTYLSRIVIFIEIVGFFIPLILNVTCSTMVLRTLNKPL
P2YR_CHICK  (190) TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKD
P2YR_MELGA  (190) TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKD
P2YR_RAT    (201) TCYDS--TSDEYLRSYFIYSMCTTVAMFCIPLVLILGCYGLIVRALIYKD
Q9Y271      (173) CFEPP--QDNQTKNHVLVLHYVSLFVGFIIPFVIIIVCYTMILTLLLKS
GPRH_HUMAN  (181) CLQLY-------REKASHHALVSLAVAFTFPFITTVTCYLLIIRSLRQGL
```

Figure 2B

```
                    251                                              300
HGPRBMY11    (217)  VPESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHL------TTWKV
HGPRBMY11v1  (233)  VPESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHL------TTWKV
P2Y5_CHICK   (213)  TLSRNKLS-KKKVLKMIFVHLVIFCFCFVPYNITLILYSLMR--TQTWIN
P2YR_CHICK   (238)  LDNSPLR---RKSIYLVIIVLTVEAVSYLPFHVMKTLNLRARLDFQTPQM
P2YR_MELGA   (238)  LDNSPLR---RKSIYLVIIVLTVEAVSYLPFHVMKTLNLRARLDFQTPQM
P2YR_RAT     (249)  LDNSPLR---RKSIYLVIIVLTVEAVSYIPFHVMKTMNLRARLDFQTPEM
Q9Y271       (221)  MKKNLSS--HKKAIGMIMVVTAAFLVSFMPYHIQRTIHLHFLHN--ETKP
GPRH_HUMAN   (224)  RVEKRLK---TKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYR--SHGAS


                    301                                              350
HGPRBMY11    (261)  GLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQ
HGPRBMY11v1  (277)  GLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQ
P2Y5_CHICK   (260)  CSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSDINSELDK--KQQ--VH
P2YR_CHICK   (285)  CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR
P2YR_MELGA   (285)  CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR
P2YR_RAT     (296)  CDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKASRR
Q9Y271       (267)  CDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRLS-TFRKHSLS
GPRH_HUMAN   (269)  CATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLK


                    351                       379
HGPRBMY11    (311)  KAK-TKCVFPVSVWLRKETRV--------
HGPRBMY11v1  (327)  KAK-TKCVFPVSVWLRKETRV--------
P2Y5_CHICK   (306)  QNT-------------------------
P2YR_CHICK   (335)  SEP-NVQSKSEEMTLNILTEYKQNGDTSL
P2YR_MELGA   (335)  SEP-NVQSKSEEMTLNILTEYKQNGDTSL
P2YR_RAT     (346)  SEA-NLQSKSEEMTLNILSEFKQNGDTSL
Q9Y271       (316)  SVT-YVPRKKASLPEKGEEICKV------
GPRH_HUMAN   (319)  GPPPSFEGKTNESSLSAKSEL--------
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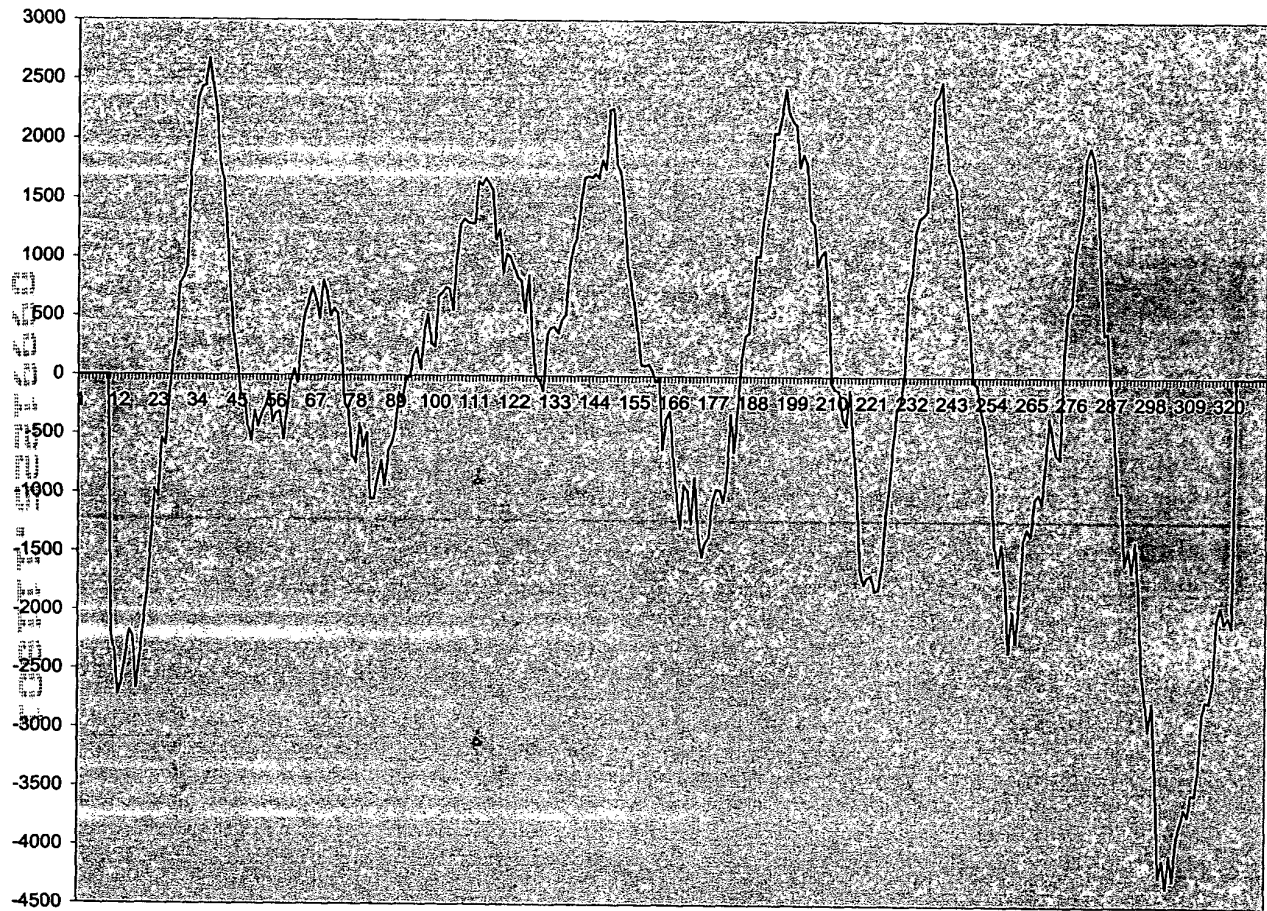
Figure 3

Figure 4.

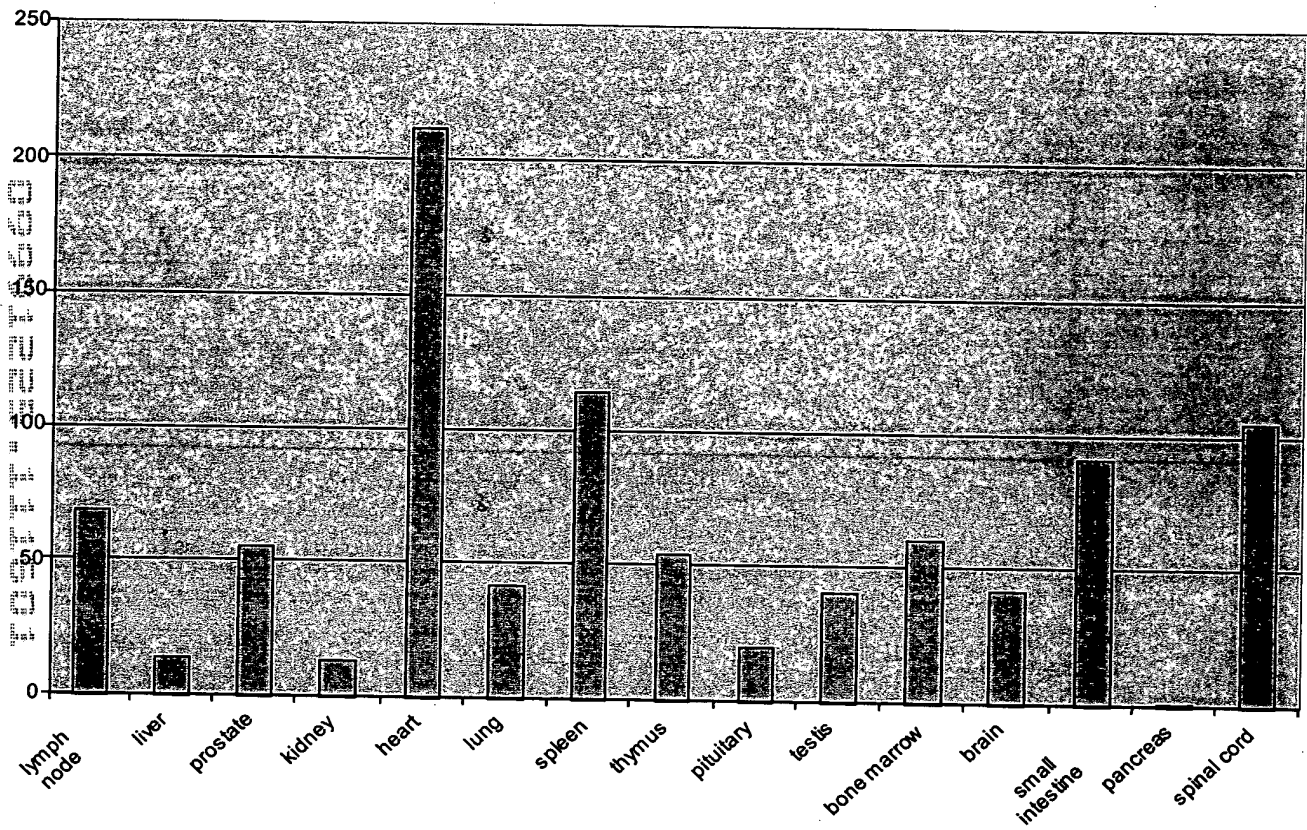**Expression Profiling of Novel Human GPCR, HGPRBMY11**

Figure 5.

HGPRBMY11

Protein	Genbank ID	Identities	Similarities
human cysteinyl leukotriene receptor	gi|11422069	37%	49%
chick purinergic receptor 5	gi|P32250	36%	46%
human G-protein-coupled receptor GPR17	gi|Q13304	36%	46%
chick purinergic receptor	gi|P34996	30%	45%
turkey purinergic receptor	gi|P49652	30%	45%
rat purinergic receptor	gi|P49651	30%	44%

HGPRBMY11v1

Protein	Genbank ID	Identities	Similarities
human cysteinyl leukotriene receptor	gi|11422069	37.2%	49%
chick purinergic receptor 5	gi|P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi|Q13304	36.2%	46.1%
chick purinergic receptor	gi|P34996	29.5%	43.9%
turkey purinergic receptor	gi|P49652	29.8%	44.2%
rat purinergic receptor	gi|P49651	29.6%	44%

Figure 6A

```
  1  ATGGAGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT   60
  1   M   E   R   K   F   M   S   L   Q   P   S   I   S   V   S   E   M   E   P   N    20


 61  GGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTT  120
 21   G   T   F   S   N   N   N   S   R   N   C   T   I   E   N   F   K   R   E   F    40


121  TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA  180
 41   F   P   I   V   Y   L   I   I   F   W   G   V   L   G   N   G   L   S   I        60


181  TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG  240
 61   Y   V   F   L   Q   P   Y   K   K   S   T   S   V   N   V   F   M   L   N   L    80


241  GCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA  300
 81   A   I   S   D   L   L   F   I   S   T   L   P   F   R   A   D   Y   Y   L   R   100


301  GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC  360
101   G   S   N   W   I   F   G   D   L   A   C   R   I   M   S   Y   S   L   Y   V   120


361  AACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATG  420
121   N   M   Y   S   S   I   Y   F   L   T   V   L   S   V   V   R   F   L   A   M   140


421  GTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG  480
141   V   H   P   F   R   L   L   H   V   T   S   I   R   S   A   W   I   L   C   G   160


481  ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG  540
161   I   I   W   I   L   I   M   A   S   S   I   M   L   L   D   S   G   S   E   Q   180


541  AACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC  600
181   N   G   S   V   T   S   C   L   E   L   N   L   Y   K   I   A   K   L   Q   T   200


601  ATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGT  660
201   M   N   Y   I   A   L   V   V   G   C   L   L   P   F   F   T   L   S   I   C   220


661  TATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTT  720
221   Y   L   L   I   I   R   V   L   L   K   V   E   V   P   E   S   G   L   R   V   240


721  TCTCACAGGAAGGCACTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTC  780
241   S   H   R   K   A   L   T   T   I   I   I   T   L   I   I   F   F   L   C   F   260


781  CTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAA  840
261   L   P   Y   H   T   L   R   T   V   H   L   T   T   W   K   V   G   L   C   K   280


841  GACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTC  900
281   D   R   L   H   K   A   L   V   I   T   L   A   L   A   A   A   N   A   C   F   300
```
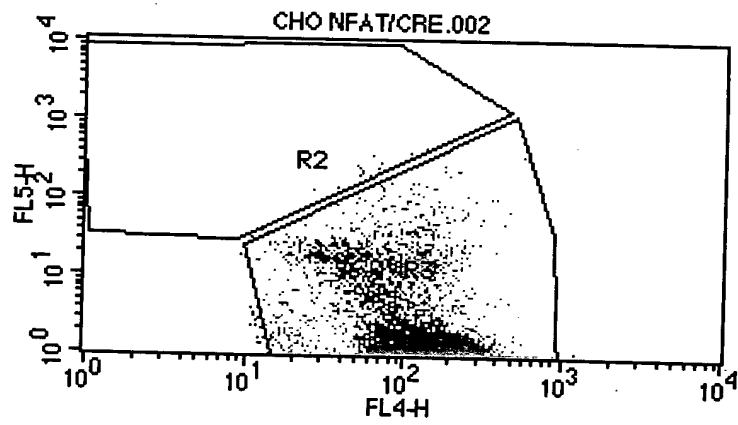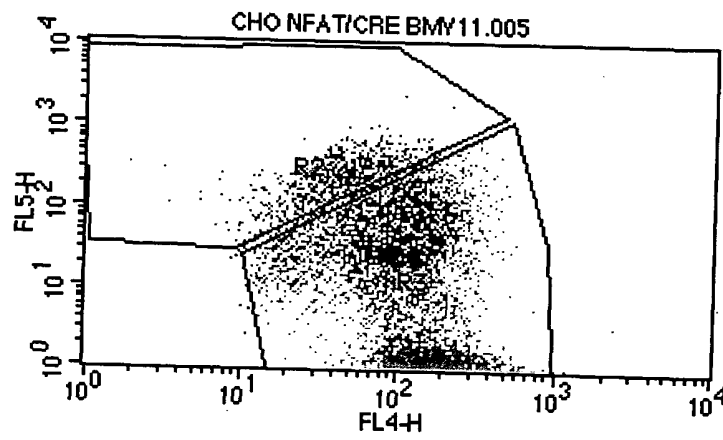
Figure 6B

```
901  AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTC   960
301   N  P  L  L  Y  Y  F  A  G  E  N  F  K  D  R  L  K  S  A  L    320
```

```
961  AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTG   1020
321   R  K  G  H  P  Q  K  A  K  T  K  C  V  F  P  V  S  V  W  L    340
```

```
1021  AGAAAGGAAACAAGAGTATAA   1041
341   R  K  E  T  R  V       346
```
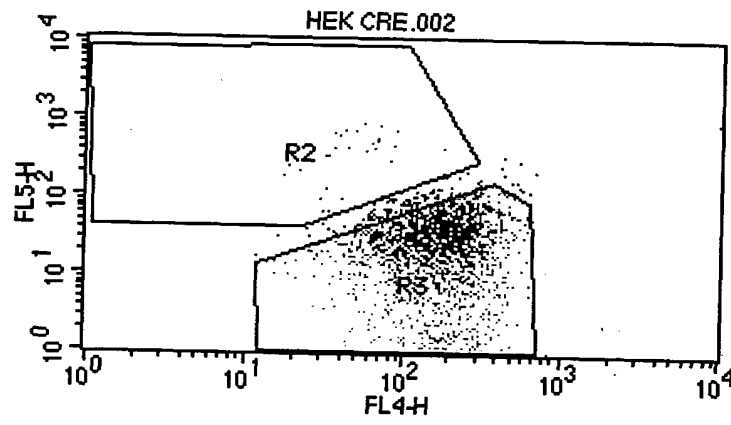
Figure 7

Figure 8

Figure 9

Figure 10
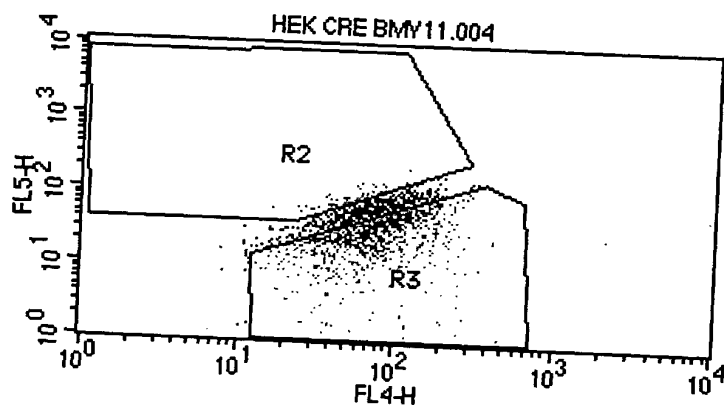
Figure 11
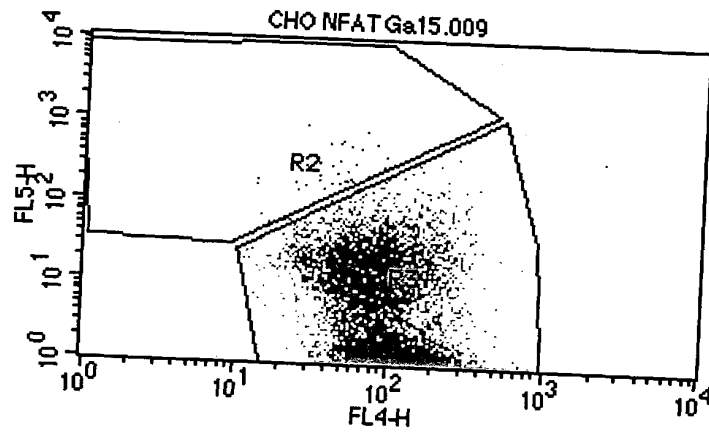
Figure 12
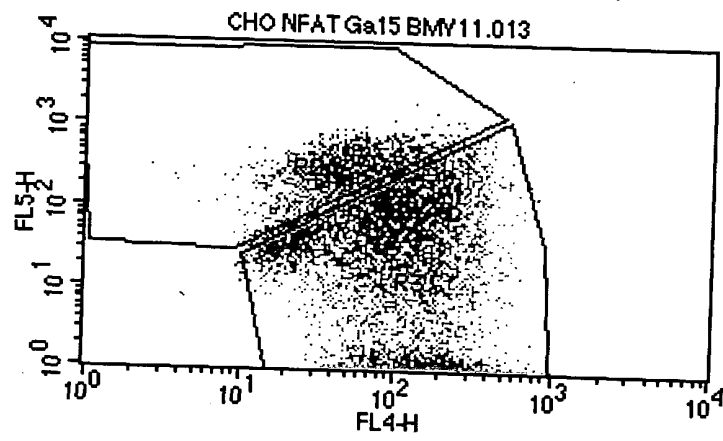
Figure 13

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)
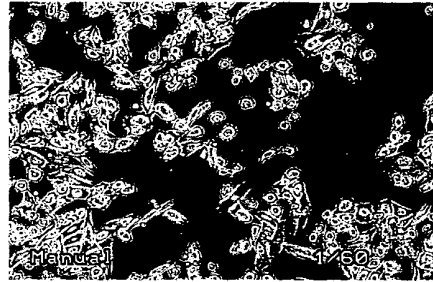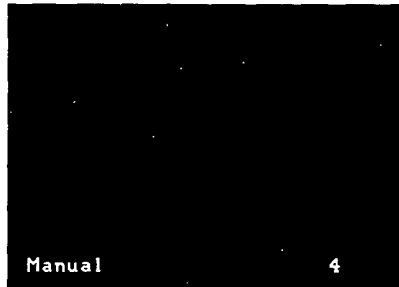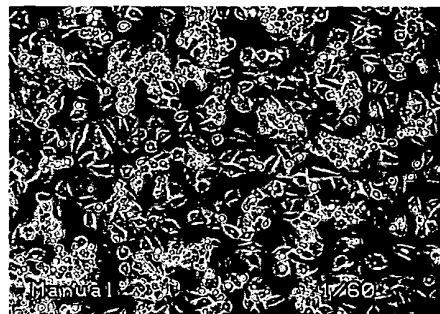

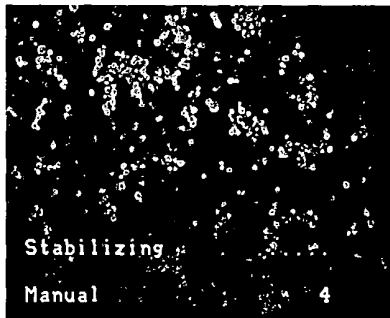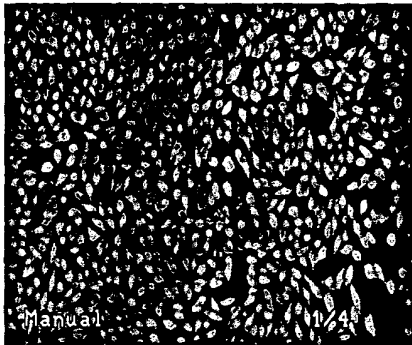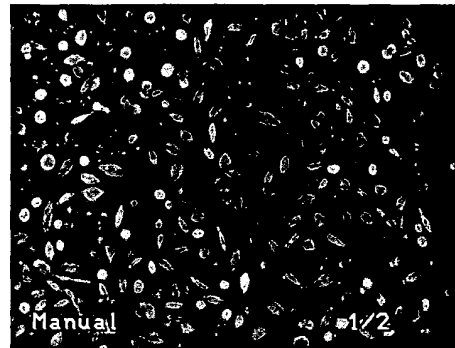Cho NFAT Ga15 BMY11 (Fluorescent vs. Bright Field)
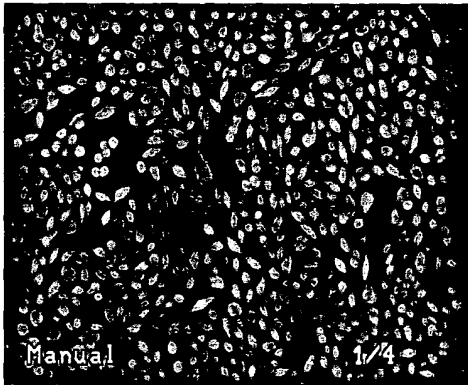
Figure 14

a. Cho-NFAT CRE

b. Cho-NFAT CRE + F/T/P

c. Cho-NFAT CRE oGPCR-Intermediate

d. Cho-NFAT CRE oGPCR High
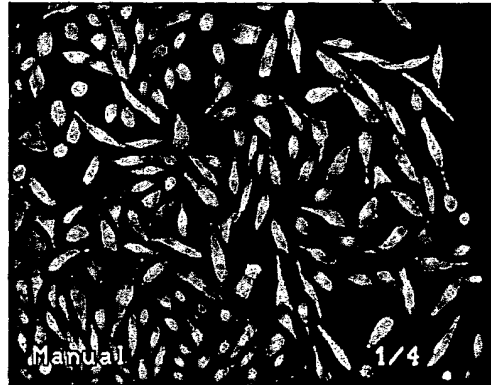
Figure 15A

```
  1  ATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT   60
  1  M   S   L   Q   P   S   I   S   V   S   E   M   E   P   N   G   T   F   S   N    20

 61  AACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTTTTCCCAATTGTATAT  120
 21  N   N   S   R   N   C   T   I   E   N   F   K   R   E   F   F   P   I   V   Y    40

121  CTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCCTGCAG  180
 41  L   I   I   F   F   W   G   V   L   G   N   G   L   S   I   Y   V   F   L   Q    60

181  CCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCTC  240
 61  P   Y   K   K   S   T   S   V   N   V   F   M   L   N   L   A   I   S   D   L    80

241  CTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA  300
 81  L   F   I   S   T   L   P   F   R   A   D   Y   Y   L   R   G   S   N   W   I   100

301  TTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAGT  360
101  F   G   D   L   A   C   R   I   M   S   Y   S   L   Y   V   N   M   Y   S   S   120

361  ATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGG  420
121  I   Y   F   L   T   V   L   S   V   V   R   F   L   A   M   V   H   P   F   R   140

421  CTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT  480
141  L   L   H   V   T   S   I   R   S   A   W   I   L   C   G   I   I   W   I   L   160

481  ATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCACA  540
161  I   M   A   S   S   I   M   L   L   D   S   G   S   E   Q   N   G   S   V   T   180

541  TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGCC  600
181  S   C   L   E   L   N   L   Y   K   I   A   K   L   Q   T   M   N   Y   I   A   200

601  TTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATT  660
201  L   V   V   G   C   L   L   P   F   F   T   L   S   I   C   Y   L   L   I   I   220

661  CGGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCA  720
221  R   V   L   L   K   V   E   V   P   E   S   G   L   R   V   S   H   R   K   A   240

721  CTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTCCTGCCCTATCACACA  780
241  L   T   T   I   I   I   T   L   I   I   F   F   L   C   F   L   P   Y   H   T   260

781  CTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAA  840
261  L   R   T   V   H   L   T   T   W   K   V   G   L   C   K   D   R   L   H   K   280

841  GCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTAT  900
281  A   L   V   I   T   L   A   L   A   A   A   N   A   C   F   N   P   L   L   Y   300
```

Figure 15B

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901  TACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA  960
301  Y  F  A  G  E  N  F  K  D  R  L  K  S  A  L  R  K  G  H  P   320


961  CAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAGA  1020
321  Q  K  A  K  T  K  C  V  F  P  V  S  V  W  L  R  K  E  T  R   340


1021 GTATAA  1026
341  V      341
```